



112766-140 (DIV-016CIP).ST25

SEQUENCE LISTING

<110> Short, Jay
Mathur, Eric
Richardson, Toby
Robertson, Dan
Barton, Nelson

<120> Recombinant Phytases and Uses Thereof

<130> 112766.140 (DIV-016CIP)

<140> US 10/021,723

<141> 2001-12-12

<150> US 60/255,090

<151> 2000-12-12

<160> 74

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1325

<212> DNA

<213> Yersinia pestis

<220>

<221> misc_feature

<222> 470, 487, 491, 492, 522

<223> n = A,T,C or G

<400> 1

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atthttgagtc gccatggtgt tcgctcgccg accaaacaaa cgcagcttat gaatgatgtt 180
acgccagata agtggccaca atggccggta aaagcgggggt atttaacgcc acgtgggtgcg 240
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cgcttaaccg gacaggcatt tcttgatggg gtggctccgg ggtgtgggtt gaccgtgcat 420
aatcaggccg atttgaaaaa gaccgatccc ctgttccatc cggtagaggn tggcgtgtgt 480
aagttanacg nngcacaaac agataaagcg attgaagaac anttgggcgg gccgttagat 540
acgggtgagcc agcgctacgc taaacctttt gccagatgg gggacgtgct gaattttgcg 600
gcttctcctt attgcaaate tttgcaacag caaggaaaaa cgtgtgattt tgccactttg 660
cggccaatga agttaacgtt aataaagaag ggacaaaagt gaccctcagt gggccactgg 720
cgttatcatc gacattgggt gaaatcttct tattacaaaa cgcacaagcc atgccagagg 780
ttgcctggca acggctaaaa ggggcggaga attgggtatc cttattgtca ttacataacg 840
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cgggtatgct gggagccgac tggcagctac ccgagcaacc tgataatact ccaccagggtg 1080
ggggattggg ttttgaacta tggcaaaatc cggataacca ccagcgctac gttgcggtga 1140
agatgttcta ccaaacgatg gatcagttgc gtaatgccga aaaattggat ctgaaaaata 1200
acccagcggg tattatttcc gttgcagttg ctggttggtga aaataacggg gacgataagc 1260
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<210> 2
 <211> 441
 <212> PRT
 <213> *Yersinia pestis*

<220>
 <221> VARIANT
 <222> 157, 163, 164, 174
 <223> Xaa = Any Amino Acid

<400> 2

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 20          25          30
Gly Tyr Thr Leu Glu Arg Val Val Ile Leu Ser Arg His Gly Val Arg
 35          40          45
Ser Pro Thr Lys Gln Thr Gln Leu Met Asn Asp Val Thr Pro Asp Lys
 50          55          60
Trp Pro Gln Trp Pro Val Lys Ala Gly Tyr Leu Thr Pro Arg Gly Ala
 65          70          75          80
Glu Leu Val Thr Leu Met Gly Gly Phe Tyr Gly Asp Tyr Phe Arg Ser
 85          90          95
Leu Gly Leu Leu Ala Ala Gly Cys Pro Ala Glu Gly Gly Val Tyr Ala
 100          105          110
Gln Ala Asp Ile Asp Gln Arg Thr Arg Leu Thr Gly Gln Ala Phe Leu
 115          120          125
Asp Gly Val Ala Pro Gly Cys Gly Leu Thr Val His Asn Gln Ala Asp
 130          135          140
Leu Lys Lys Thr Asp Pro Leu Phe His Pro Val Glu Xaa Gly Val Cys
 145          150          155          160
Lys Leu Xaa Xaa Ala Gln Thr Asp Lys Ala Ile Glu Glu Xaa Leu Gly
 165          170          175
Gly Pro Leu Asp Thr Val Ser Gln Arg Tyr Ala Lys Pro Phe Ala Gln
 180          185          190
Met Gly Asp Val Leu Asn Phe Ala Ala Ser Pro Tyr Cys Lys Ser Leu
 195          200          205
Gln Gln Gln Gly Lys Thr Cys Asp Phe Ala His Phe Ala Ala Asn Glu
 210          215          220
Val Asn Val Asn Lys Glu Gly Thr Lys Val Thr Leu Ser Gly Pro Leu
 225          230          235          240
Ala Leu Ser Ser Thr Leu Gly Glu Ile Phe Leu Leu Gln Asn Ala Gln
 245          250          255
Ala Met Pro Glu Val Ala Trp Gln Arg Leu Lys Gly Ala Glu Asn Trp
 260          265          270
Val Ser Leu Leu Ser Leu His Asn Ala Gln Phe Asn Leu Met Ala Lys
 275          280          285
Thr Pro Tyr Ile Ala Arg His Lys Gly Thr Pro Leu Leu Gln Gln Ile
 290          295          300
Asp Thr Ala Leu Thr Leu Gln Leu Asp Ala Gln Gly Gln Lys Leu Pro
 305          310          315          320
Ile Ser Ala Gln Asn Arg Val Leu Phe Leu Gly Gly His Asp Thr Asn
 325          330          335
Ile Ala Asn Ile Ala Gly Met Leu Gly Ala Asp Trp Gln Leu Pro Glu
 340          345          350
Gln Pro Asp Asn Thr Pro Pro Gly Gly Leu Val Phe Glu Leu Trp
 355          360          365
Gln Asn Pro Asp Asn His Gln Arg Tyr Val Ala Val Lys Met Phe Tyr

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      370              375              380
Gln Thr Met Asp Gln Leu Arg Asn Ala Glu Lys Leu Asp Leu Lys Asn
385              390              395              400
Asn Pro Ala Gly Ile Ile Ser Val Ala Val Ala Gly Cys Glu Asn Asn
      405              410              415
Gly Asp Asp Lys Leu Cys Glu Leu Asp Thr Phe Gln Lys Lys Val Ala
      420              425              430
Lys Val Ile Glu Pro Ala Cys His Ile
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<210> 3
 <211> 1325
 <212> DNA
 <213> *Yersinia pestis*

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<400> 3
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atthttgagtc gccatgggtgt tgcctcgccg accaaacaac gcagcttatg aatgatgtta 180
cgccagataa gtggccacaa tggccggtaa aagcggggta tttaacgcca cgtgggtcgg 240
agttggtcac attgatgggg ggggttttatg gtgattactt tcgcagcctt ggtttgtag 300
cggcgggatg tccggcagag ggggggggtat atgcacaggc agatatcgat caacgtaccc 360
gcttaaccgg acaggcattt cttgatgggt tggctccggg gtgtggtttg accgtgcata 420
atcaggccga tttgaaaaag accgatcccc tgttccatcc ggtagagact ggcgtgtgta 480
agttagacaa cgcacaaaca gataaagcga ttgaagaacg attgggcggg ccgtagata 540
cggtagacca ggcgtacgct aaaccttttg ccagatggg ggacgtgctg aattttgcgg 600
cttctcctta ttgcaaatct ttgcaacagc aaggaaaaac gtgtgatttt gccactttg 660
cggccaatga agttaacggt aataaagaag ggacaaaagt gaccctcagt gggccactgg 720
cgttatcatc gacattgggt gaaatcttct tattacaaaa cgcacaagcc atgccagagg 780
ttgcctggca acggctaaaa ggggcggaga attgggtatc cttattgtca ttacataacg 840
cgcaatttaa tttaatggca aaaacaccgt atatcgcccg tcataaaggg acgccattat 900
tacagcagat agatacggct ttaacccttc aactggatgc tcaggggcaa aagctaccca 960
tttcagccca aaaccgggtc ttgttctctg gtgggcatga taccaatatt gccaatattg 1020
cgggtatgct gggagccgac tggcagctac ccgagcaacc tgataaact ccaccagggtg 1080
ggggattggg ttttgaacta tggcaaaatc cggataacca ccagcgctac gttgcgggtga 1140
agatgttcta ccaaacgatg gatcagttgc gtaatgccga aaaattggat ctgaaaaata 1200
accagcggg tattatttcc gttgcagttg ctggttgtga aaataacggg gacgataagc 1260
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tctaa

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<210> 4
 <211> 420
 <212> PRT
 <213> *Yersinia pestis*

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<400> 4
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Leu Ser Gly Leu Ala Ala Ile Thr Ala Pro Val Ala Ala Glu Pro Ser
      20              25              30
Gly Tyr Thr Leu Glu Arg Val Val Ile Leu Ser Arg His Gly Val Arg
      35              40              45
Ser Pro Thr Lys Gln Thr Gln Leu Met Asn Asp Val Thr Pro Asp Lys
      50              55              60
Trp Pro Gln Trp Pro Val Lys Ala Gly Tyr Leu Thr Pro Arg Gly Ala
65              70              75              80
Glu Leu Val Thr Leu Met Gly Gly Phe Tyr Gly Asp Tyr Phe Arg Ser

```



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gtcctcaagg caagctacaa ggagcgacg atcgcgaccg cgcagaactg ggccgcgggg 420
ttcatgcccg gctgcacggc ggatgtcgcg catcccgccg gtccggacga tgacgcgac 480
tttcatgggc tcgacggcgg ccccgctcgt ttcgacggca agcgggcatt cgatgcccg 540
ctcgcccagg cggccgaggg cgggctgacc gccgaaaccg cacgccatcg cggcgaactg 600
accttgctcg cgaaagtgtc gaattgtgcg ctgcccgcct gcccgctgat cgccgagccg 660
agccgactgg tcgcgcagcc gcacgatcgc cccgatctcg aaggcccgct cgacgtcgga 720
tcgaccgcca gccagacgct ggtgctggaa tatctggaag gcaagccgat ggccgaggtc 780
ggctggggcc gcgtaagccg cggcgagatc gagcagttgc tgcgctttca tccgctcaaa 840
ttcgcgtatt cgaatcgccc cggctatata gccgcgcgcg ccgcggcgcc gatcgtgcgc 900
gaaatcgttg cggcgctcga cagcaacagc ccggcgcggc tgaccttgct cgccgggcac 960
gacacgaacg tcgccgacct cggcggttct ttcgacctgc actggcaggt gccgagctat 1020
cccgcgcgag aggttcgcgc cggcagcgcg ttggggttcg agctggtcag caacgcgaag 1080
ggcgaccgct atgtccgcgc cttctatcgc gcgcagacga tggaccagct ccgcaacctc 1140
gaaccgctgg ggtcgggtga cgcgctgtac cgccgctatc ttcccattcc ggggtgcggc 1200
cattcggtcg aggcgaaccg gtgcagctgg agtgatttcg cccggctcgc cgccgcgcgc 1260
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<210> 6

<211> 421

<212> PRT

<213> Artificial Sequence

<220>

<223> 953-6 phytase sequence

<400> 6

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 1           5           10          15
Leu Leu Leu Ser Ala Ala Leu Leu Ala Gly Cys Ala Ala Ser Ala Pro
 20          25          30
Gly Ala Asp Ala Ser Pro Ala Ala Pro Gly Ser Leu Lys Leu Glu Lys
 35          40          45
Val Val Met Leu Met Arg His Gly Val Arg Pro Pro Thr Lys Ala Ala
 50          55          60
Val Val Pro Pro Gly Tyr Ser Ala Glu Thr Trp Pro Asp Trp Pro Val
 65          70          75          80
Asp Phe Gly Leu Leu Thr Pro His Gly Ala Ala Gly Val Lys Leu Leu
 85          90          95
Gly Glu Ser Asp Arg Leu Thr Phe Gly Gly Arg Gly Leu Phe Pro Asp
100         105         110
Gly Cys Pro Ala Ala Gly Thr Ile Val Leu Lys Ala Ser Tyr Lys Glu
115         120         125
Arg Thr Ile Ala Thr Ala Gln Asn Trp Ala Ala Gly Phe Met Pro Gly
130         135         140
Cys Thr Ala Asp Val Ala His Pro Ala Gly Pro Asp Asp Ala Ile
145         150         155         160
Phe His Gly Leu Asp Gly Gly Pro Ala Ser Phe Asp Gly Lys Arg Ala
165         170         175
Phe Asp Ala Ala Leu Ala Gln Ala Pro Glu Gly Gly Leu Thr Ala Glu
180         185         190
Thr Ala Arg His Arg Gly Glu Leu Thr Leu Leu Ala Lys Val Leu Asn
195         200         205
Cys Ala Leu Pro Ala Cys Pro Leu Ile Ala Glu Pro Ser Arg Leu Val
210         215         220
Ala Gln Pro His Asp Arg Pro Asp Leu Glu Gly Pro Leu Asp Val Gly
225         230         235         240

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<210> 7
<211> 1230
<212> DNA
<213> Rhizobium
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<210> 8
<211> 409
<212> PRT
<213> Rhizobium
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<400> 8

Val Lys His Ser Leu Leu Leu Pro Ala Ala Leu Leu Ala Gly Cys Ala
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 Ala Ser Ala Pro Gly Ala Cys Ala Ser Pro Ala Ala Pro Gly Ser Leu
 20 25 30
 Lys Leu Glu Lys Val Val Met Leu Met Arg His Gly Val Arg Pro Pro
 35 40 45
 Thr Lys Ala Ala Val Val Pro Pro Gly Tyr Ser Ala Glu Thr Trp Pro
 50 55 60
 Asp Trp Pro Val Asp Phe Gly Leu Leu Thr Pro His Gly Ala Ala Gly
 65 70 75 80
 Val Lys Leu Leu Gly Glu Ser Asp Arg Leu Tyr Phe Gly Gly Arg Gly
 85 90 95
 Leu Phe Pro Glu Gly Cys Pro Ala Ala Gly Thr Ile Val Leu Lys Ala
 100 105 110
 Ser Tyr Lys Glu Arg Thr Ile Ala Thr Ala Gln Ser Trp Ala Ala Gly
 115 120 125
 Phe Met Pro Gly Cys Ala Thr Asp Val Ala His Pro Ala Gly Pro Asp
 130 135 140
 Asp Asp Ala Ile Phe His Gly Leu Asp Gly Gly Pro Ala Ser Phe Asp
 145 150 155 160
 Gly Lys Arg Ala Phe Asp Ala Ala Leu Ala Gln Ala Pro Glu Gly Gly
 165 170 175
 Leu Thr Ala Glu Thr Ala Arg His Arg Gly Glu Leu Thr Leu Leu Ala
 180 185 190
 Lys Val Leu Asn Cys Ala Leu Pro Ala Cys Pro Leu Ile Ala Glu Pro
 195 200 205
 Ser Arg Leu Val Ala Gln Pro His Asp Arg Pro Glu Ile Glu Gly Pro
 210 215 220
 Leu Asp Val Gly Ser Thr Ala Ser Gln Thr Leu Val Leu Glu Tyr Leu
 225 230 235 240
 Glu Gly Lys Pro Met Ala Glu Val Gly Trp Gly Arg Val Ser Arg Ala
 245 250 255
 Glu Ile Glu Gln Leu Leu Arg Phe His Pro Leu Lys Phe Arg Tyr Ser
 260 265 270
 Asn Arg Pro Gly Tyr Ile Ala Ala Thr Ala Ala Ala Pro Ile Val Arg
 275 280 285
 Glu Ile Val Thr Ala Leu Gly Asp Arg Ser Pro Ala Arg Leu Thr Leu
 290 295 300
 Leu Ala Gly His Asp Thr Asn Val Ala Asp Leu Gly Gly Phe Phe Asp
 305 310 315 320
 Leu His Trp Gln Val Pro Ser Tyr Pro Ala Asp Glu Val Pro Pro Gly
 325 330 335
 Ser Ala Leu Gly Phe Glu Leu Val Ser Asn Ala Lys Gly Asp Arg Tyr
 340 345 350
 Val Arg Ala Phe Tyr Arg Gly Gln Thr Met Asp Gln Leu Arg Asn Leu
 355 360 365
 Glu Pro Leu Arg Ser Asp Asp Thr Leu Phe Arg Arg Tyr Leu Pro Ile
 370 375 380
 Pro Gly Cys Gly Asn Ser Val Glu Ala Thr Ala Cys Ala Trp Ser Asp
 385 390 395 400
 Phe Ala Arg Leu Ala Ala Pro Arg Gly
 405

<210> 9

<211> 1431

<212> DNA

<213> Artificial Sequence

<220>

<223> 954-2 phytase sequence

<400> 9

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gcgggtagcg agccgccccg gaaggccgcg gcaacagatg gcatgccgca agactgggctg 180
ctcgacgcgt tggatcatcg cagccggcac ggcgtgcggt ctccgacgcg tccggagccg 240
ccgctggaga gcctcagccc cgatccgtgg ccccagtggt ccgtgccgac tgcccacctg 300
accgatcgtg gcgcggcgct cgtctcgcag atggggcggt actacggtga ttggcttcgt 360
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gacgttgacc agcggaccgc tctgacgggc gacgcctgc tcctcggcat ggcgcaggc 480
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atggaatcgg gtgcatgccc agtcgacccc gtacaggcga agcgcgacat cgaagcgcat 600
gccggcgagg gcggcggtgg gacactggga aggcgtacg cagcaagcct gaccagaatg 660
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<210> 10

<211> 476

<212> PRT

<213> Artificial Sequence

<220>

<223> 954-2 phytase sequence

<400> 10

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Met Lys Lys Thr Ile Trp Arg Arg Val Gly Gln Arg Trp Arg Arg Gly
 1           5           10           15
Ala Cys Ala Ala Thr Val Leu Leu Ser Ala Cys Ser Thr Gln Leu Pro
 20           25           30
Gly Val Pro Ala Thr Leu Ser Ala Ala Gly Ser Glu Pro Pro Arg Lys
 35           40           45
Ala Ala Ala Thr Asp Gly Met Pro Gln Asp Trp Ser Leu Asp Ala Leu
 50           55           60
Val Ile Val Ser Arg His Gly Val Arg Ser Pro Thr Arg Pro Glu Pro
 65           70           75           80
Pro Leu Glu Ser Leu Ser Pro Asp Pro Trp Pro Gln Trp Pro Val Pro
 85           90           95
Thr Ala His Leu Thr Asp Arg Gly Ala Ala Leu Val Ser Gln Met Gly
100           105           110
Arg Tyr Tyr Gly Asp Trp Leu Arg Ala Arg Gly Val Leu Pro Ala Ser
115           120           125
Gly Cys Pro Ala Thr Gly Thr Leu Tyr Gly Trp Ala Asp Val Asp Gln

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130	135	140
Arg Thr Arg Leu Thr Gly Asp Ala Leu Leu Leu Gly Met Ala Pro Gly		
145	150	155
Cys Gly Ile His Ser Asp His Arg Ala Ala Leu Asp Glu Lys Asp Pro		160
	165	170
Ile Phe His Ala Met Glu Ser Gly Ala Cys Pro Val Asp Pro Val Gln		175
	180	185
Ala Lys Arg Asp Ile Glu Ala His Ala Gly Glu Gly Gly Val Ala Thr		190
	195	200
Leu Gly Arg Arg Tyr Ala Ala Ser Leu Thr Arg Met Ser Glu Val Leu		205
	210	215
Asp Tyr Ala His Ser Ala Asp Cys Ala Arg His Gly Gly Gln Cys Asp		220
225	230	235
Tyr Ala Arg Gln Pro Asn Arg Val Glu Ile Arg Pro Asp Gly Leu His		240
	245	250
Ala Ala Leu Lys Gly Pro Met Gly Ser Ala Ser Thr Val Ser Glu Val		255
	260	265
Phe Leu Leu Glu His Gly Gln Gly Leu Pro Gln Glu Gln Val Ala Trp		270
	275	280
Gly Arg Ile His Asp Ala Gln Asp Trp Thr Leu Leu Met Gln Ala His		285
	290	295
Asn Ala Gln Phe Asp Leu Met Ala Lys Thr Pro Tyr Met Ala Thr Arg		300
305	310	315
Arg Gly Thr Pro Met Leu Ala Ser Val Leu Asp Ala Leu Glu Arg Arg		320
	325	330
Ala Gly Ala Pro Ala Pro Glu Leu Ala Val Lys Gly Pro Lys Leu Pro		335
	340	345
Gln Gly Asn Arg Val Tyr Val Leu Thr Ala His Asp Thr Asn Leu Ala		350
	355	360
His Leu Ala Gly Leu Leu His Leu Asp Trp Thr Leu Pro Glu Gln Pro		365
	370	375
Asp Asp Thr Pro Pro Gly Gly Ala Met Val Phe Ser Leu Trp Arg Glu		380
385	390	395
Pro Gly Thr Gln Ala Arg Phe Val Arg Val Glu Met Val Tyr Gln Ser		400
	405	410
Met Asp Gln Leu Arg Gln Leu Thr Pro Leu Ser Leu Ala Gln Pro Pro		415
	420	425
His Arg Leu Ile Leu Pro Leu Pro Gly Cys Ala Asp Ala Ala His Gly		430
	435	440
His Ala Cys Ser Leu Pro Glu Phe Ser Arg Arg Val Arg Ala Ala Leu		445
	450	455
Ser Pro Ser Cys Leu Glu Ala Val Thr Ala Ala His		460
465	470	475

<210> 11

<211> 1326

<212> DNA

<213> Yersinia pestis

<400> 11

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attttgagtc gccatggtgt gcgtagcccg actaagcaga cgcagctgat gaatgatgta 180
acacctgata agtggcctca gtggccgggt aaagcgggct atttgactcc tcgtggcgcc 240
gaactggcca cctgatggg cgggttctat ggcgattatt tccgcagttt gggctctttg 300
gcccggggtt gcccggcaga gggcgggtga tatgcacagg cagatatcga ccagcgact 360
cgtttaaccg gtcaggcttt tctggatggt gtggcgccgg gttgcggcct gactgtccac 420

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aatcaggccg atcttaagaa aaccgatcct ctgtttcatc ccgttgaaac cggcgtctgt 480
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gcgagtccgt actgcaagtc actgcagcag caggggaaaa cttgtgactt cgcacacttt 660
gcgccaacg aagttaatgt aaacaaggaa ggcacgaaag ttaccctgtc aggccccctg 720
gcgctgtcta gcacgttggg cgaaatcttc ttgctgcaga acgcgcaggc gatgcccga 780
gtagcgtggc agcgtttgaa aggcgctgag aactgggtgt ctcttctgag cctgcacaat 840
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gccggtatgc tgggcgcaga ttggcagtta ccggaacaac cggataacac cccaccgggc 1080
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aagatgttct atcagaccat ggatcaattg cgtaacgccg agaagctgga tttaaagaac 1200
aatcccgccg gcatcatcag tgctcgtgtg gccggtgcg agaataatgg tgacgataaa 1260
ctgtgcgaac ttgatacttt tcaaaaaaaa gtagcgaag tcattgaacc tgcgtgtcat 1320
atctaa
1326

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<210> 12

<211> 441

<212> PRT

<213> *Yersinia pestis*

<400> 12

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Met Ser Gly Leu Glu Asn Arg Val Arg Leu Ser Gly Leu Val Leu Met
1          5          10          15
Leu Ser Gly Leu Ala Ala Ile Thr Ala Pro Val Ala Ala Glu Pro Ser
20          25          30
Gly Tyr Thr Leu Glu Arg Val Val Ile Leu Ser Arg His Gly Val Arg
35          40          45
Ser Pro Thr Lys Gln Thr Gln Leu Met Asn Asp Val Thr Pro Asp Lys
50          55          60
Trp Pro Gln Trp Pro Val Lys Ala Gly Tyr Leu Thr Pro Arg Gly Ala
65          70          75          80
Glu Leu Val Thr Leu Met Gly Gly Phe Tyr Gly Asp Tyr Phe Arg Ser
85          90          95
Leu Gly Leu Leu Ala Ala Gly Cys Pro Ala Glu Gly Gly Val Tyr Ala
100          105          110
Gln Ala Asp Ile Asp Gln Arg Thr Arg Leu Thr Gly Gln Ala Phe Leu
115          120          125
Asp Gly Val Ala Pro Gly Cys Gly Leu Thr Val His Asn Gln Ala Asp
130          135          140
Leu Lys Lys Thr Asp Pro Leu Phe His Pro Val Glu Thr Gly Val Cys
145          150          155          160
Lys Leu Asp Asn Ala Gln Thr Asp Lys Ala Ile Glu Glu Arg Leu Gly
165          170          175
Gly Pro Leu Asp Thr Val Ser Gln Arg Tyr Ala Lys Pro Phe Ala Gln
180          185          190
Met Gly Asp Val Leu Asn Phe Ala Ala Ser Pro Tyr Cys Lys Ser Leu
195          200          205
Gln Gln Gln Gly Lys Thr Cys Asp Phe Ala His Phe Ala Ala Asn Glu
210          215          220
Val Asn Val Asn Lys Glu Gly Thr Lys Val Thr Leu Ser Gly Pro Leu
225          230          235          240
Ala Leu Ser Ser Thr Leu Gly Glu Ile Phe Leu Leu Gln Asn Ala Gln
245          250          255
Ala Met Pro Glu Val Ala Trp Gln Arg Leu Lys Gly Ala Glu Asn Trp
260          265          270
Val Ser Leu Leu Ser Leu His Asn Ala Gln Phe Asn Leu Met Ala Lys

```

```

      275      280      285
Thr Pro Tyr Ile Ala Arg His Lys Gly Thr Pro Leu Leu Gln Gln Ile
 290      295      300
Asp Thr Ala Leu Thr Leu Gln Leu Asp Ala Gln Gly Gln Lys Leu Pro
305      310      315      320
Ile Ser Ala Gln Asn Arg Val Leu Phe Leu Gly Gly His Asp Thr Asn
      325      330      335
Ile Ala Asn Ile Ala Gly Met Leu Gly Ala Asp Trp Gln Leu Pro Glu
      340      345      350
Gln Pro Asp Asn Thr Pro Pro Gly Gly Gly Leu Val Phe Glu Leu Trp
      355      360      365
Gln Asn Pro Asp Asn His Gln Arg Tyr Val Ala Val Lys Met Phe Tyr
      370      375      380
Gln Thr Met Asp Gln Leu Arg Asn Ala Glu Lys Leu Asp Leu Lys Asn
385      390      395      400
Asn Pro Ala Gly Ile Ser Val Ala Val Ala Gly Cys Glu Asn Asn
      405      410      415
Gly Asp Asp Lys Leu Cys Glu Leu Asp Thr Phe Gln Lys Lys Val Ala
      420      425      430
Lys Val Ile Glu Pro Ala Cys His Ile
      435      440

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<210> 13
 <211> 410
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> amino acid sequence of a phytase enzyme with
 predicted glycosylation sites

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<400> 13
Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser Val Val Ile Val Ser Arg
 1      5      10      15
His Gly Val Arg Ala Pro Thr Lys Ala Thr Gln Leu Met Gln Asp Val
      20      25      30
Thr Pro Asp Ala Trp Pro Thr Trp Pro Val Lys Leu Gly Glu Leu Thr
      35      40      45
Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu Gly His Tyr Trp Arg Gln
      50      55      60
Arg Leu Val Ala Asp Gly Leu Leu Pro Lys Cys Gly Cys Pro Gln Ser
65      70      75      80
Gly Gln Val Ala Ile Ile Ala Asp Val Asp Glu Arg Thr Arg Lys Thr
      85      90      95
Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro Asp Cys Ala Ile Thr Val
      100      105      110
His Thr Gln Ala Asp Thr Ser Ser Pro Asp Pro Leu Phe Asn Pro Leu
      115      120      125
Lys Thr Gly Val Cys Gln Leu Asp Asn Ala Asn Val Thr Asp Ala Ile
      130      135      140
Leu Glu Arg Ala Gly Gly Ser Ile Ala Asp Phe Thr Gly His Tyr Gln
145      150      155      160
Thr Ala Phe Arg Glu Leu Glu Arg Val Leu Asn Phe Pro Gln Ser Asn
      165      170      175
Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu Ser Cys Ser Leu Thr Gln
      180      185      190
Ala Leu Pro Ser Glu Leu Lys Val Ser Ala Asp Cys Val Ser Leu Thr

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<220>
<223> consensus sequence

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Cys Ala Arg Val Val Gly Arg Leu Gly Pro Leu Leu Ala Ser Thr Leu
                165                170                175
Ser Glu Ile Phe Leu Leu Glu Tyr Ala Gln Gly Pro Met Glu Val Gly
                180                185                190
Trp Gly Arg Ile Ser Ala Glu Trp Leu Leu His Asn Ala Gln Phe Leu
                195                200                205
Met Asn Arg Thr Pro Tyr Ile Ala Arg Ala Thr Pro Ile Leu Ile Val
                210                215                220
Thr Ala Leu Ser Pro Ala Arg Val Val Leu Leu Ala Gly His Asp Thr
                225                230                235                240
Asn Leu Ala Leu Gly Gly Leu Asp Leu Trp Gln Leu Pro Gln Pro Asp
                245                250                255
Glu Thr Pro Pro Gly Gly Ala Leu Val Phe Glu Leu Trp Asn Arg Tyr
                260                265                270
Val Arg Val Met Tyr Gln Thr Met Asp Gln Leu Arg Asn Leu Glu Pro
                275                280                285
Leu Leu Pro Arg Ile Leu Pro Ile Pro Gly Cys Gly Ser Glu Ala Ala
                290                295                300
Cys Ser Leu Ser Asp Phe Ala Arg Leu Val Ala Pro Ala Cys
305                310                315

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<210> 15
 <211> 410
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> amino acid sequence of a phytase enzyme with
 predicted glycosylation sites

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<400> 15
Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser Val Val Ile Val Ser Arg
 1                5                10                15
His Gly Val Arg Ala Pro Thr Lys Ala Thr Gln Leu Met Gln Asp Val
                20                25                30
Thr Pro Asp Ala Trp Pro Thr Trp Pro Val Lys Leu Gly Glu Leu Thr
                35                40                45
Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu Gly His Tyr Trp Arg Gln
                50                55                60
Arg Leu Val Ala Asp Gly Leu Leu Pro Lys Cys Gly Cys Pro Gln Ser
65                70                75                80
Gly Gln Val Ala Ile Ile Ala Asp Val Asp Glu Arg Thr Arg Lys Thr
                85                90                95
Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro Asp Cys Ala Ile Thr Val
                100                105                110
His Thr Gln Ala Asp Thr Ser Ser Pro Asp Pro Leu Phe Asn Pro Leu
                115                120                125
Lys Thr Gly Val Cys Gln Leu Asp Asn Ala Asn Val Thr Asp Ala Ile
                130                135                140
Leu Glu Arg Ala Gly Gly Ser Ile Ala Asp Phe Thr Gly His Tyr Gln
145                150                155                160
Thr Ala Phe Arg Glu Leu Glu Arg Val Leu Asn Phe Pro Gln Ser Asn
                165                170                175
Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu Ser Cys Ser Leu Thr Gln
                180                185                190
Ala Leu Pro Ser Glu Leu Lys Val Ser Ala Asp Cys Val Ser Leu Thr
                195                200                205

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Gly Ala Val Ser Leu Ala Ser Met Leu Thr Glu Ile Phe Leu Leu Gln
 210                215                220
Gln Ala Gln Gly Met Pro Glu Pro Gly Trp Gly Arg Ile Thr Asp Ser
225                230                235                240
His Gln Trp Asn Thr Leu Leu Ser Leu His Asn Ala Gln Phe Asp Leu
                245                250                255
Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg Ala Thr Pro Leu Leu
                260                265                270
Asp Leu Ile Lys Thr Ala Leu Thr Pro His Pro Pro Gln Lys Gln Ala
                275                280                285
Tyr Gly Val Thr Leu Pro Thr Ser Val Leu Phe Ile Ala Gly His Asp
290                295                300
Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu Glu Leu Asn Trp Thr Leu
305                310                315                320
Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly Glu Leu Val Phe Glu
                325                330                335
Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln Trp Ile Gln Val Ser Leu
                340                345                350
Val Phe Gln Thr Leu Gln Gln Met Arg Asp Lys Thr Pro Leu Ser Leu
                355                360                365
Asn Thr Pro Pro Gly Glu Val Lys Leu Thr Leu Ala Gly Cys Glu Glu
370                375                380
Arg Asn Ala Gln Gly Met Cys Ser Leu Ala Gly Phe Thr Gln Ile Val
385                390                395                400
Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
                405                410

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<210> 16
 <211> 432
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> appa phytase sequence

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<400> 16
Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr
 1                5                10                15
Pro Gln Ser Ala Phe Ala Gln Ser Glu Arg Glu Leu Lys Leu Glu Ser
                20                25                30
Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
                35                40                45
Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Thr Val
50                55                60
Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
65                70                75                80
Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys
                85                90                95
Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
100                105                110
Glu Lys Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro
115                120                125
Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Gly
130                135                140
Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala
145                150                155                160
Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp

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				165					170					175			
Phe	Thr	Gly	His	Arg	Gln	Thr	Ala	Phe	Arg	Glu	Leu	Glu	Arg	Val	Leu		
			180					185					190				
Asn	Phe	Pro	Gln	Ser	Asn	Leu	Cys	Leu	Lys	Arg	Glu	Lys	Gln	Asp	Glu		
		195					200					205					
Ser	Cys	Ser	Leu	Thr	Gln	Ala	Leu	Pro	Ser	Glu	Leu	Lys	Val	Ser	Ala		
	210				215						220						
Asp	Asn	Val	Ser	Leu	Thr	Gly	Ala	Val	Ser	Leu	Ala	Ser	Met	Leu	Thr		
225					230					235					240		
Glu	Ile	Phe	Leu	Leu	Gln	Gln	Ala	Gln	Gly	Met	Pro	Glu	Pro	Gly	Trp		
			245						250					255			
Gly	Lys	Ile	Thr	Asp	Ser	His	Gln	Trp	Asn	Thr	Leu	Leu	Ser	Leu	Leu		
			260					265					270				
Asn	Ala	Gln	Phe	Tyr	Leu	Leu	Gln	Arg	Thr	Pro	Glu	Val	Ala	Arg	Ser		
	275						280					285					
Arg	Ala	Thr	Pro	Leu	Leu	Asp	Leu	Ile	Lys	Thr	Ala	Leu	Thr	Pro	His		
	290					295					300						
Pro	Pro	Gln	Lys	Gln	Ala	Tyr	Gly	Val	Thr	Leu	Pro	Thr	Ser	Val	Leu		
305					310					315					320		
Phe	Ile	Ala	Gly	His	Asp	Thr	Trp	Leu	Ala	Asn	Leu	Gly	Gly	Ala	Leu		
			325					330						335			
Glu	Leu	Asn	Trp	Thr	Leu	Pro	Gly	Gln	Pro	Asp	Asn	Thr	Pro	Pro	Gly		
		340					345						350				
Gly	Glu	Leu	Val	Phe	Glu	Arg	Trp	Arg	Arg	Leu	Ser	Asp	Asn	Ser	Gln		
		355					360					365					
Trp	Ile	Gln	Val	Ser	Leu	Val	Phe	Gln	Thr	Leu	Gln	Gln	Met	Asp	Asp		
	370					375					380						
Lys	Thr	Pro	Leu	Ser	Leu	Asn	Thr	Pro	Pro	Gly	Glu	Val	Lys	Leu	Thr		
385					390					395					400		
Leu	Ala	Gly	Cys	Glu	Glu	Arg	Asn	Ala	Gln	Gly	Met	Gln	Ser	Leu	Ala		
			405					410					415				
Gly	Phe	Thr	Gln	Ile	Val	Asn	Glu	Ala	Arg	Ile	Pro	Ala	Cys	Ser	Leu		
			420					425					430				

<210> 17

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> first region of a phytate sequence

<220>

<221> VARIANT

<222> 6

<223> Xaa = Any Amino Acid

<400> 17

Arg His Gly Val Arg Xaa Pro Thr

1

5

<210> 18

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> second region of a phytate sequence

<220>

<221> VARIANT

<222> 3

<223> Xaa = Any Amino Acid

<400> 18

Trp Pro Xaa Trp Pro Val

1

5

<210> 19

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 19

cttctactag aattcattaa agaggagaaa ttaaccatgt ccgtactgga gaa 53

<210> 20

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 20

ccgcgtccgc ctttccgggt tagtgtaaat gctgtccggc ctggctgc 48

<210> 21

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 21

tatcacccgc cctgtggccg ccgaaccatc ggggtacacc ttagaacgtg tag 53

<210> 22

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 22
 ttattttgag tcgccatggt gtgcgtagcc cgactaagca gacgcagctg atgaa 55

<210> 23
 <211> 64
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for the construction of Yersinia
 pestis phytase

<400> 23
 tgatgtaaca cctgataagt ggcctcagtg gccgggtaaa gcgggctatt tgactcctcg 60
 tggc 64

<210> 24
 <211> 67
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for the construction of Yersinia
 pestis phytase

<400> 24
 gccgaactgg tcaccctgat gggcgggttc tatggcgatt atttccgcag tttgggtctt 60
 ttggccg 67

<210> 25
 <211> 56
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for the construction of Yersinia
 pestis phytase

<400> 25
 gccgcgggct gcccggcaga gggcgggtga tatgcacagg cagatatcga ccagcg 56

<210> 26
 <211> 55
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for the construction of Yersinia
 pestis phytase

<400> 26
 cactcgttta accggtcagg cttttctgga tgggtgtggcg ccgggttgcg gcctg 55

<210> 27
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 27

actgtccaca atcaggccga tcttaagaaa accgatactc tgtttcatcc 50

<210> 28

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 28

cgttgaaacc ggcgtctgta aactggacaa cgcccaaacc gataaggcaa ttga 54

<210> 29

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 29

ggaacgcctg ggcggcccgt tagacacggt aagccagcgc tatgccaaac cgtttgcg 58

<210> 30

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 30

caaatgggcg atgtcctgaa cttcgctgcg agtccgtact gcaagtcact gcagcagcag 60
gggaaaa 67

<210> 31

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 31

aaaacttggt acttcgcaca ctttgcggcc aacgaagtta atgtaaacia ggaag 55

<210> 32

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 32

gcacgaaagt tacctgtca ggccccctgg cgctgtctag cacgttgggc gaaatctt 58

<210> 33

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 33

cttgctgcag aacgcgcagg cgatgccga agtagcgtgg cagcgtttga aaggcgct 58

<210> 34

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 34

gagaactggg tgtctcttct gagcctgcac aatgcacagt tcaacctgat ggctaaaa 58

<210> 35

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 35

cgccatacat tgcacgccac aaaggcacgc cgcttttaca gcaaactgat accgcactga 60

<210> 36

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 36

ccctgcaact ggacgccag gggcaaaaac tgccgatctc ggctcagaac cgtgttttat 60

tcctgggtg

69

<210> 37

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 37

ggtggccacg acacaaatat tgctaacatc gccggtatgc tgggcgcaga ttggcagtta 60
c 61

<210> 38

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 38

cggaacaacc ggataacacc ccaccgggcg gcggtctggt ctttgagctg tggcagaat 59

<210> 39

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

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pestis phytase

<400> 39

ccggacaatc atcaacgtta tgtggccggt aagatgttct atcagaccat ggat 54

<210> 40

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 40

caactgcgta acgccgagaa gctggattta aagaacaatc ccgccggcat catcagtg 58

<210> 41

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia

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<400> 41
tcgctgtggc cggctgcgag aataatgggtg acgataaact gtgcgaactt g 51

<210> 42
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 42
atacttttca aaaaaaagta gcgaaagtca ttgaacctgc gtgtcatatt aaagcttcta 60
ctacta 66

<210> 43
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 43
agtagtagaa gcttaaatat gac 23

<210> 44
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 44
acgcggttct ccagtagcga catggttaat ttctcctctt taatgaattc tagtagaag 59

<210> 45
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 45
ggtgatagca gccaggccgg acagcattaa cactaaaccg gaaaggcgg 49

<210> 46
<211> 53
<212> DNA
<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 46

aaaataacta cacgtttctaa ggtgtacccc gatggttcgg cggccacagg cgc 53

<210> 47

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 47

acatcattca tcagctgcgt ctgcttagtc gggctacgca caccatggcg actc 54

<210> 48

<211> 62

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 48

cggcgccacg aggagtcaaa tagcccgctt taaccggcca ctgaggccac ttatcaggtg 60
tt 62

<210> 49

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 49

cggccaaaag acccaaactg cggaaataat cgccatagaa cccgcccac agggtgacca 60
ggt 63

<210> 50

<211> 62

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 50

cgagtgcgct ggtcgatatc tgctgtgca tatacacgc cctctgccgg gcagcccgcg 60
gc 62

<210> 51
 <211> 55
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide for the construction of Yersinia
 pestis phytase

 <400> 51
 gacagtcagg ccgcaacccg gcgccacacc atccagaaaa gcctgaccgg ttaaa 55

 <210> 52
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide for the construction of Yersinia
 pestis phytase

 <400> 52
 tcaacgggat gaaacagagg atcggttttc ttaagatcgg cctgattgtg 50

 <210> 53
 <211> 55
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide for the construction of Yersinia
 pestis phytase

 <400> 53
 gcgttctca attgccttat cggtttgggc gttgtccagt ttacagacgc cggtt 55

 <210> 54
 <211> 58
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide for the construction of Yersinia
 pestis phytase

 <400> 54
 ccatttgcgc aaacggtttg gcatagcgct ggcttaccgt gtctaacggg ccgcccag 58

 <210> 55
 <211> 60
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide for the construction of Yersinia
 pestis phytase

 <400> 55

ttttccctg ctgctgcagt gacttgcaat acggactcgc agcgaagttc aggacatcgc 60

<210> 56

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 56

tcgtgccttc cttgtttaca ttaacttcgt tggccgcaaa gtgtgcgaag tcacaagttt 60
t 61

<210> 57

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 57

agcaagaaga tttcgcccaa cgtgctagac agcgccaggg ggctgacag ggtaactt 58

<210> 58

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 58

gttctcagcg cctttcaaac gctgccacgc tacttcgggc atcgctgcg cgttctgc 58

<210> 59

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 59

atggcgtttt agccatcagg ttgaactgtg cattgtgcag gctcagaaga gacaccca 58

<210> 60

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 60
gcagggtcag tgcggtatcg atttgctgta aaagcggcgt gcctttgtgg cgtgcaatgt 60

<210> 61
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 61
caccaggaa taaaacacgg ttctgagccg agatcggcag tttttgcccc tgggcgtcca 60
ggt 63

<210> 62
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 62
gttccggtaa ctgccaatct gcgcccagca taccggcgat gttagcaata tttgtgtcgt 60
ggccacc 67

<210> 63
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 63
gtccggattc tgccacagct caaagaccag accgccgccc ggtgggggtgt tatccggtt 59

<210> 64
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide for the construction of Yersinia
pestis phytase

<400> 64
gcagttgatc catggtctga tagaacatct taacggccac ataacgttga tgatt 55

<210> 65
<211> 57

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide for the construction of Yersinia
 pestis phytase

 <400> 65
 cagcgacact gatgatgccg gcgggattgt tctttaaatc cagcttctcg gcgttac 57

 <210> 66
 <211> 51
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide for the construction of Yersinia
 pestis phytase

 <400> 66
 aagtatcaag ttcgcacagt ttatcgtcac cattattctc gcagccggcc a 51

 <210> 67
 <211> 60
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide for the construction of Yersinia
 pestis phytase

 <400> 67
 tagtagtaga agctttaata tgacacgcag gttcaatgac tttcgctact tttttttgaa 60

 <210> 68
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 68
 ctactagaat tcattaaaga ggag 24

 <210> 69
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 69
 tactgacgtc tcacggccaa aagacccaaa ctgcg 35

 <210> 70

<211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 70
 tactgacgtc tcagccgcgg gctgcccggc agagg 35

<210> 71
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 71
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